

241 AAVLVTLILGLIVFGIMFAYSRGHFDRTRKGTSSKKVIYSOPS-----ARSEGEF 291
 303 RHKSSEFV 310
 : : : :
 292 KOTSSFLV 299

RESULT 2

neural cell adhesion molecule 1 - African clawed frog

JE0099

N/Alternate names: NCAM-1

C/Species: Xenopus laevis (African clawed frog)

C/Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000

C/Accession: JE0099

R/Kudo, M.; Takayama, E.; Tadokuma, T.; Shiohawa, K.

Biochem. Biophys. Res. Commun. 245, 127-132, 1998

A/Title: Molecular cloning of sdb-form neural cell adhesion molecules (N-CAMs) as the ma

A/Reference number: JE0099; MUID:98204770; PMID:9535795

A/Accession: JE0099

A/Molecule type: mRNA

A/Residues: 1-725 <KUD>

A/Cross-references: DDBJ:AB008162; NID:g3116226; PIDN:BA25931.1; PID:g3116227

A/Experimental source: heart

C/Comment: This protein mediates and regulates various cell-cell interactions through bc

C/Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

F/413-475/Domain: immunoglobulin homology <IMM>

F/512-589/Domain: fibronectin type III repeat homology <3FR>

Query Match 11.4%; Score 187; DB 2; Length 725;

Best Local Similarity 29.9%; Pred. No. 1.6e-07;

Matches 63; Conservative 30; Mismatches 82; Indels 36; Gaps 12;

30 GAVNLK-----SNRTPVQEFSEVELSCITDSDPR-IEWK-KIODEQTTFVFPDN 82

105 GTVNLKIYQKLTFRKAPRPFQEFKEGDAVITICDVSSISPIITWRHKGKD-----VIFKK 159

83 KIQGLDLAGRAEILGKTSIKIMWTRDSALYRCE--VVARND--RKEIDEIV-IELTVQV 137

160 DV-----RFVLLANNVYQIRGIKKTDEGTYRCEGRILARGEINVKDQIVVNPPTQA 213

QY 138 KPTTPVCPKAVPVGKATLHCQSESGHPRPHYSWRNDVLPDTSRANPRFNSSHL 197

214 RQL-----RVNATANNAESVVLSC-DADGFPDPPEISMLKKGEP-EDGEKISF----- 260

DB 198 NSETGLVFTAVHKDGGQYVCIASNDGSA 228

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

DB 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

QY 261 NEDQSEMTIHVEKDEAEYSCLANNQAGEA 291

F1542/Binding site: substrate phosphate (Arg) #status predicted
F1826/Active site: Cys (phosphocysteine intermediate) #status predicted
F1832/Binding site: substrate phosphate (Arg) #status predicted

Query Match 11.0%; Score 180.5; DB 2; Length 1894;

Best Local Similarity 28.8%; Pred. No. 1.7e-06;
Matches 72; Conservative 34; Mismatches 75; Indels 69; Gaps 15;

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QY 3 LRRPRLRL-----CARLPDFLLLFRCGLIGAVNLKSSRTYVVOEFSEVLSCTIT 56
DB 11 VRRPRLSLTLFLPLCAETPRPF-----TRTVDTQTGVSQVASTFC 52
QY 57 DSQTSDFR--IEW-----KKIQDEQTTTFYFNDKIQDLAGRAELIKTSLKIMNTRRDS 110
DB 53 QA-TDDPRKIVMKNKKKVSQNGREVEIEFD-----GSGSVLRIOPLR-----TPRDE 100
QY 111 ALYREVAARNDKRIDELIVELTVQKVPYVCAVPKAVPVGK-----ATL 158
DB 101 AIYEC--VASNNGBI-SVSTRITVLRBD-----QIPRPFPTIDMGPOLKVERTRTATM 152
QY 159 HQSESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSHNSSET-GTIVFTAVHKDSSGOY 217
DB 153 LCAAS-GNPDEPITWFKPLPVDI-SNNNGRIK---QIRSESIGALQIEGSESDQGY 206
QY 218 YCIASNDGS 227
DB 207 ECVATNSAGT 216

```

RESULT 5

A11923
amalgam protein precursor - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster
C/Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 21-Jul-2000
C/Accession: A11923
R/Seeger, M.A.; Halfley, L.; Kaufman, T.C.
Cell 55, 589-600, 1988
A/Title: Characterization of amalgam: a member of the immunoglobulin superfamily from D.
A/Reference number: A11923; MUID:89028670; PMID:3141062
A/Accession: A11923
A/Molecule type: DNA
A/Residues: 1-333-<SEB>
A/Cross-references: GB:M23561; NID:G156920; PIDN:AAA28367.1; PID:G156921
C/Genetics:
A/Gene: FlyBase:ama
A/Cross-references: FlyBase:FBgn0000071

Query Match 11.0%; Score 180; DB 2; Length 333;
Best Local Similarity 26.8%; Pred. No. 2.3e-07;
Matches 52; Conservative 39; Mismatches 83; Indels 20; Gaps 5;

```

QY 35 KSSNTPVVOEFSEVLSCTITDSQTSDFRISWKIQDEQTTTFYFNDKIQDLAGRAEI 94
DB 143 EMTPTKSTLTVECONLELTC--HANGFPKPTISMAR-----EHNAMPAGGHL 187
QY 95 LKRTSLKIMNTRRDSALYRCVAVARNDKRIDELIVELTVQKVPYVCAVPKAVPGK 154
DB 188 LAEPFLTRRSVHRMDRGTYC--IAONGEGQPKRILRVEVERPIAIAQRPKIAQWVSH 245
QY 155 MATLHQSESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSHNSSETGTLVFTAVHKDS 214
DB 246 SALELE-SVQGYRPAITVVMHKNQVPL--QSSRHHEVAVANASSGTTTSLRLDSGDEDF 302
QY 215 GOYYCIASNDGSA 228
DB 303 GDYYCNATKLGHA 316

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RESULT 6

JE0100
neural cell adhesion molecule 2 - African clawed frog

N/Alternate names: N-CAM 2
C/Species: Xenopus laevis (African clawed frog)

C/Date: 19-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C/Accession: JE0100
R/Kudo, M.; Takayama, E.; Tadakuma, T.; Shiohawa, K.
Biochem. Biophys. Res. Commun. 245, 127-132, 1998

A/Title: Molecular cloning of sed-form neural cell adhesion molecules (N-CAMs) as the ma
A/Reference number: JE0099; MUID:98204770; PMID:9535795
A/Accession: JE0100
A/Molecule type: mRNA
A/Residues: 1-725 <KUD>
A/Cross-references: DDBJ:AB008163; NID:G3116228; PIDN:BAA25932.1; PID:G3116229

A/Experimental source: heart
C/Comment: This protein mediates and regulates various cell-cell interactions through bc
C/Suprafamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
F/413-475/Domain: immunoglobulin homology <IMM>
F/512-589/Domain: fibronectin type III repeat homology <3FR>

Query Match 10.8%; Score 177; DB 2; Length 725;

Best Local Similarity 29.5%; Pred. No. 1.1e-06;
Matches 62; Conservative 28; Mismatches 86; Indels 34; Gaps 11;

```

QY 30 GAVNLKSSNR-----TPVVOEFSEVLSCTITDSQTSDFR-IEWK-KIQDEQTTVFYFND 82
DB 105 GTVNLKTYQKLTFFKAPPPQFTBGEADVILCDVSSISPTITWKKKD-----VIRK 159
QY 83 KIQDLAGRAELIKTSLKIMNTRRDSALYRC--VVARNDKRIDELIVELTVQKVPY 140
DB 160 DV-----RFVVLANNVLIQIRIGIKKTDEGNRCERILARG---EINVKDQIVINVPPL 210
QY 141 TPV--CRVPKAVPVGKATLHQSESEGHPRPHYSWYRNDVPLPTDSRANPRFRNSSHIN 198
DB 211 IQARQIRVNAVATAMDESIVLSC-DADGFPDEISWLKGEPI-EDGEEKISF-----N 261
QY 199 SETGLVFTAVHKDSSGOYYCIASNDGSA 228
DB 262 EDKSEMTIYRVEKEDAEYSCLANNQGEA 291

```

RESULT 7

JN0635
neural cell adhesion molecule 2 precursor - African clawed frog

C/Species: Xenopus laevis (African clawed frog)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 22-Jun-1999
C/Accession: JN0635
R/Tonissen, K.F.; Krieg, P.A.
Gene 127, 243-247, 1993

A/Title: Two neural-cell adhesion molecule (NCAM)-encoding genes in Xenopus laevis are ex
A/Reference number: JN0635; MUID:93273239; PMID:7684721
A/Accession: JN0635
A/Molecule type: mRNA
A/Residues: 1-1092 <TON>

A/Cross-references: GB:M76710; NID:G214611; PIDN:AAA49910.1; PID:G214612
C/Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C/Genetics:
A/Gene: NCAM2

C/Suprafamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu
C/Keywords: alternative splicing; cell adhesion; duplication; heparin binding; siologlyc
F/1-19/Domain: signal sequence #status predicted <SIG>
F/20-1092/Product: neural cell adhesion molecule 2 #status predicted <EXT>

F/34-95/Domain: extracellular #status predicted <EXT>
F/129-188/Domain: immunoglobulin homology <IMM2>
F/149-153/Region: heparin binding #status predicted
F/158-162/Region: heparin binding #status predicted
F/317-381/Domain: immunoglobulin homology <IMM3>

F/413-475/Domain: immunoglobulin homology <IMM4>
F/512-589/Domain: fibronectin type III repeat homology <FN3A>
F/619-680/Domain: fibronectin type III repeat homology <FN3B>
F/706-723/Domain: transmembrane #status predicted <TM>
F/724-1092/Domain: intracellular #status predicted <INT>

F/41-93,136-186,232-282,323-379,420-473/Disulfide bonds: #status predicted
F/219,310,341,417,443,472/Binding site: carbohydrate (asn) (covalent) #status predicted
Query Match 10.8%; Score 177; DB 1; Length 1092;

Best Local Similarity 29.5%; Pred. No. 1.7e-06;
Matches 62; Conservative 28; Mismatches 86; Indels 34; Gaps 11;

QY 30 GAVNLKSSNR-----TPVQEFESVLSCLITTSQTSPP-IEWK-KIQDEQTYVFPN 82
Db 105 GTVNLKTYQLTKTKVAPTPQEPFEGEDAVTICVSSISPIITWRKGDV---VIFPK 159
QY 83 KIQGDLAGRAELIGKTSLKIMNTRRDSALYRCE--VVARNDREKIDEIYELTVQKPV 140
Db 160 DV-----RFVVLANNYLQIRGKIKTDEGNRCGRIIARG---ELNYKDIOQIVVPP 210
QY 141 TPV--CRVPKAVPGKATLHCQESBGPPEPHYSWYRNDVPLTDSRANFRFNSSSHN 198
Db 211 IQARQIRVATAMDESIVLSC-DADGFPPEISMLKGEPI-EDGEKISF-----N 261
QY 199 SENGTLVFTAVHKDQSGQYCIASNDGSA 228
Db 262 EDKSEMTIYRVEKEDEAEYSCLANNOAGEA 291

RESULT 8

IUMSNG

neural cell adhesion molecule 1 precursor, GPI-anchored splice form - mouse

N:Alternate names: NCAM-120

C:Species: Mus musculus (house mouse)

C>Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 31-Dec-2000

C:Accession: A29673; S00382; A44290

R:Barthele, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fontec

EMBO J. 6, 907-914, 1987

A>Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000

A:Reference number: A29673; PMID:87246524; PMID:3595653

A:Accession: A29673

A:Molecule type: mRNA

A:Residues: 1-725 <BAR>

A:Cross-references: EMBL:Y00051; NID:G53342; PIDN:CAA68263.1; PID:G53343

R:Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.

EMBO J. 7, 625-632, 1988

A>Title: Differential splicing and alternative polyadenylation generates distinct NCAM

A:Reference number: S00382; PMID:88283628; PMID:3396534

A:Accession: S00382

A:Molecule type: DNA

A:Residues: 642-656, 'D', 656-725 <BA2>

A:Cross-references: EMBL:X07195

R:Rougon, G.; Marshak, D.R.

J. Biol. Chem. 261, 3396-3401, 1986

A>Title: Structural and immunological characterization of the amino-terminal domain of

A:Reference number: A44290; PMID:86140120; PMID:3512536

A:Accession: A44290

A:Molecule type: protein

A:Residues: 20-36 <ROU>

C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol

C:Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IMSG

C:Genetics: NCAM

A:Gene position: 9

A:introns: 701/1

C:Keyword: alternative splicing; cell adhesion; duplication; heparin binding; membrane

F:1-15/Domain: signal sequence #status predicted <SIG>

F:34-98/Domain: immunoglobulin homology <IMM1>

F:132-191/Domain: immunoglobulin homology <IMM2>

F:152-156/Region: heparin binding #status predicted

F:161-165/Region: heparin binding #status predicted

F:228-290/Domain: immunoglobulin homology <IMM3>

F:263-272/Region: NCAM binding #status predicted

F:323-388/Domain: immunoglobulin homology <IMM4>

F:420-482/Domain: immunoglobulin homology <IMM5>

F:519-596/Domain: fibronectin type III repeat homology <FN3>

F:625-685/Domain: fibronectin type III repeat homology <FN3>

F:81-96, 139-189, 235-288, 330-366, 427-480/Dissulfide bonds: #status predicted

F:222, 316, 348, 424, 450, 479/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.5%; Score 171.5; DB 1; Length 725;

Best Local Similarity 27.3%; Pred. No. 3e-06;
Matches 63; Conservative 41; Mismatches 84; Indels 43; Gaps 12;

QY 27 CLIGA-----NLKSSNR-----TPVQEFESVLSCLITTSQTS-DRIRMKIQ 71
Db 96 CVVLTADGTQSATVAVNKI PQGLMFRNAPTPEPFEGEDAVTICVSSISPIITWRKGDV---VIFPK 152
QY 72 DEQTYVFPDNKIQGDLAGRAELIGKTSLKIMNTRRDSALYRCE--VVARNDREKIDEI 129
Db 153 -----HKGRDVLTKD--RFVLNNYLLQIRGKIKTDEGNRCGRIIARG---ELNPK 202
QY 130 VIELTVQKVPVPCR--VPKAVPGKATLHCQESBGPPEPHYSWYRNDVPLTDSRAN 187
Db 203 DIQVIVNVPVQARQSIYVATANGQSVTLVC-DADGFPPEPTMWTXGPEIENEDEE-D 260
QY 188 PRFRSSSHNSNGETGVFTAVHKDQSGQYCIASNDGSAACEQMEVY 238
Db 261 ERSRSV-----SDSSEVTIRNDVKNDEARVYCIANKKG-----EQDASIH 302

RESULT 9

IUMSNT

neural cell adhesion molecule 1 precursor, long domain splice form - mouse

N:Alternate names: NCAM-180

C:Species: neural cell adhesion molecule, short domain splice form (NCAM-140)

C>Date: 31-Mar-1993 #sequence revision 31-Mar-1993 #text_change 31-Dec-2000

C:Accession: A29673; S00844; S00384; A28281; A44290; S00383

R:Barthele, D.; Santoni, M.J.; Wille, W.; Ruppert, C.; Chaix, J.C.; Hirsch, M.R.; Fontec

EMBO J. 6, 907-914, 1987

A>Title: Isolation and nucleotide sequence of mouse NCAM cDNA that codes for a Mr 79,000

A:Reference number: A29673; PMID:87246524; PMID:3595653

A:Accession: A29673

A:Molecule type: mRNA

A:Residues: 1-548, 'T', 550-571, 'T', 573-574, 'D', 576-588, 'MQB', 593, 'S', 595-599, 'P', 601, 'L'

A:Cross-references: EMBL:Y00051; NID:G53342; PIDN:CAA68263.1; PID:G53343

R:Santoni, M.J.; Barthele, D.; Barbas, J.A.; Hirsch, M.R.; Steinmetz, M.; Goridis, C.; W

Nucleic Acids Res. 15, 8621-8641, 1987

A>Title: Analysis of cDNA clones that code for the transmembrane forms of the mouse neur

A:Reference number: S00844; PMID:88067687; PMID:3684567

A:Accession: S00844

A:Molecule type: mRNA

A:Residues: 529-809, 1077-1115 <SNA>

A:Cross-references: EMBL:X06328; NID:G53322; PIDN:CAA29641.1; PID:G817984

R:Barbas, J.A.; Chaix, J.C.; Steinmetz, M.; Goridis, C.

EMBO J. 7, 625-632, 1988

A>Title: Differential splicing and alternative polyadenylation generates distinct NCAM

A:Reference number: S00382; PMID:88283628; PMID:3396534

A:Accession: S00384

A:Molecule type: DNA

A:Residues: 642-1115 <BAR>

A:Cross-references: EMBL:X07195

R:Barthele, D.; Vopper, G.; Wille, W.

Nucleic Acids Res. 16, 4217-4225, 1988

A>Title: NCAM-180, the large isoform of the neural cell adhesion molecule of the mouse,

A:Reference number: A28281; PMID:88247737; PMID:2454455

A:Accession: A28281

A:Molecule type: mRNA

A:Residues: 804-1081 <BA3>

A:Cross-references: EMBL:X07244; NID:G53321; PIDN:CAA30230.1; PID:G929720

R:Rougon, G.; Marshak, D.R.

J. Biol. Chem. 261, 3396-3401, 1986

A>Title: Structural and immunological characterization of the amino-terminal domain of m

A:Reference number: A44290; PMID:86140120; PMID:3512536

A:Accession: A44290

A:Molecule type: protein

A:Residues: 20-36 <ROU>

C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol

C:Comment: Several forms of NCAM are produced by alternative splicing. See also PIR:IMSG

C:Genetics: NCAM

A:Gene position: 9

A:introns: 643/3; 701/1; 770/2; 809/2; 1076/2

C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin-like fold
C:Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; signal sequence
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-115/Product: neural cell adhesion molecule, long domain splice form #status expert
F:20-809/1077-1115/Product: neural cell adhesion molecule, short domain splice form #status expert
F:34-98/Domain: extracellular #status predicted <EXT>
F:132-191/Domain: immunoglobulin homology <IMM1>
F:151-165/Region: heparin binding #status predicted
F:161-165/Region: heparin binding #status predicted
F:128-290/Domain: immunoglobulin homology <IMM2>
F:152-156/Region: heparin binding #status predicted
F:161-165/Region: heparin binding #status predicted
F:132-388/Domain: NCAM binding #status predicted <IMM4>
F:420-482/Domain: immunoglobulin homology <IMM5>
F:519-556/Domain: fibronectin type III repeat homology <FN3A>
F:625-685/Domain: fibronectin type III repeat homology <FN3B>
F:712-729/Domain: transmembrane #status predicted <TM>
F:730-1115/Domain: intracellular #status predicted <INT>
F:41-96,139-189,235-288,330-386,427-480/Dissulfide bonds: #status predicted
F:222,316,348,424,450,479/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.5%; Score 171.5; DB 1; Length 1115;
Best Local Similarity 27.3%; Pred. No. 5e-06;
Matches 63; Conservative 41; Mismatches 84; Indels 43; Gaps 12;

Qy 27 CLIGA-----VNLSNR-----TPVQEFSEVSLCITDSOTS-DPRIEMKIQ 71
Db 96 CVVTAEDGTQSEATVAVNVKIFQKLMFNKAPTPQEFKEGSDAVYCDVSSLPPTIWK--- 152
Qy 72 DEQTYVFPFNKIQGLDLAGRAEILGKTSIKIWNTRDSALYRCE--VVARNDKEIDEI 129
Db 153 -----HKGRDVLTKDV--RPIVLSNNYLIQIRGKIKTDEGTREGRIILANG--EINFK 202
Qy 130 VIELTVQKPTVPCR--VPRKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRAN 187
Db 203 DIQYIVNVPPTVQARQSIIVANATANGOSVTLVC--DADGPEPTMSWTGDEPIENEE--D 260
Qy 188 PRFRNSSHLNSETGLVFTAVHKDQSGQYCIASNDGASARCEQEMEYV 238
Db 261 EKSRSV---SDSSEVTIRNVDKNDKDEAEVYCIANKAG-----EDDASIH 302

RESULT 10
neural cell adhesion molecule short domain form precursor - rat
N/Alternate names: NCAM-140
C/Species: Rattus norvegicus (Norway rat)
C/Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 22-Jun-1999
C/Accession: S00846; B37795; I58136
R/Small, S.J., Shull, G.E., Santoni, M.J.; Akesson, R.
J. Cell Biol. 105, 2335-2345, 1987
A/Title: Identification of a cDNA clone that contains the complete coding sequence for a
A/Reference number: S00846; MUID:88059265; PMID:3680385
A/Accession: S00846
A/Molecule type: mRNA
A/Residues: 1-858 <SMA>
A/Cross-references: EMBL:X06564
R/Small, S.J.; Akesson, R.
J. Cell Biol. 111, 2089-2096, 1990
A/Title: Expression of the unique NCAM VASE exon is independently regulated in distinct
A/Reference number: A37795; MUID:91035620; PMID:1699951
A/Accession: B37795
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 340-381 <SM2>
R/Small, S.J.; Haines, S.L.; Akesson, R.A.
Neuron 1, 1007-1017, 1988
A/Title: Polypeptide variation in an N-CAM extracellular immunoglobulin-like fold is de
A/Reference number: I58136; MUID:90166485; PMID:2483093
A/Accession: I58136
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 355-364 <RES>

A/Cross-references: GB:M32611; NID:g205643; PIDN:AAA4679.1; PID:g205644
C/Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol
C/Comment: Various forms of NCAM are produced by alternative splicing.
A/Genes: NCAM
C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immunoglobulin-like fold
C:Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; signal sequence
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-858/Product: neural cell adhesion molecule, short domain form #status predicted <MA
F:20-721/Domain: extracellular #status predicted <EXT>
F:34-98/Domain: immunoglobulin homology <IMM1>
F:132-191/Domain: immunoglobulin homology <IMM2>
F:152-156/Region: heparin binding #status predicted
F:161-165/Region: heparin binding #status predicted
F:128-290/Domain: immunoglobulin homology <IMM3>
F:263-272/Region: NCAM binding #status predicted
F:323-358/Domain: immunoglobulin homology <IMM4>
F:430-492/Domain: immunoglobulin homology <IMM5>
F:529-606/Domain: fibronectin type III repeat homology <FN3A>
F:635-695/Domain: fibronectin type III repeat homology <FN3B>
F:722-739/Domain: transmembrane #status predicted <TM>
F:740-858/Domain: intracellular #status predicted <INT>
F:41-96,139-189,235-288,330-396,437-450/Dissulfide bonds: #status predicted
F:222,316,348,434,460,489/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 10.4%; Score 170.5; DB 1; Length 858;
Best Local Similarity 26.3%; Pred. No. 4.5e-06;
Matches 61; Conservative 41; Mismatches 85; Indels 45; Gaps 12;

Qy 27 CLIGA-----VNLSNR-----TPVQEFSEVSLCITDSOTS-DPRIEMKIQ 71
Db 96 CVVTAEDGTQSEATVAVNVKIFQKLMFNKAPTPQEFKEGSDAVYCDVSSLPPTIWK--- 152
Qy 72 DEQTYVFPFNKIQGLDLAGRAEILGKTSIKIWNTRDSALYRCE--VVARNDKEIDEI 129
Db 153 -----HKGRDVLTKDV--RPIVLSNNYLIQIRGKIKTDEGTREGRIILANG--EINFK 202
Qy 130 VIELTVQKPTVPCR--VPRKAVPVGKMATLHCQSEGHPRPHYSWYRNDVPLPTDSRAN 187
Db 203 DIQYIVNVPPTVQARQSIIVANATANGOSVTLVC--DADGPEPTMSWTGDEPIENEE--D 258
Qy 188 PRFRNSSHLNSETGLVFTAVHKDQSGQYCIASNDGASARCEQEMEYV 238
Db 259 ---EDDEKHIFSDSDSSELTIRNVDKNDKDEAEVYCIANKAG-----EDDASIH 302

RESULT 11
A56178
protein-tyrosine-phosphatase (EC 3.1.3.48), receptor type delta precursor - huma
N/Alternate names: protein-tyrosine-phosphatase Bpp-2
C/Species: Homo sapiens (man)
C/Date: 03-Oct-1995 #sequence revision 03-Oct-1995 #text_change 21-Jan-2000
C/Accession: A56178; S12052; B44929
R/Pulido, R.; Krueger, N.X.; Serra-Pages, C.; Saito, H.; Streuli, M.
J. Biol. Chem. 270, 6722-6728, 1995
A/Title: Molecular characterization of the human transmembrane protein-tyrosine phosphat
ase delta isoform.
A/Reference number: A56178; MUID:95204468; PMID:7896816
A/Accession: A56178
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1912 <PUL>
A/Cross-references: GB:I38929; NID:g755652; PIDN:AAC41749.1; PID:g755653
R/Krueger, N.X.; Streuli, M.; Saito, H.
EMBO J. 9, 3241-3252, 1990
A/Title: Structural diversity and evolution of human receptor-like protein tyrosine phos
A/Reference number: S12052; MUID:9106018; PMID:2170109
A/Accession: S12052
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 390-1912 <KRU>
A/Cross-references: GB:X54133; NID:g35789; PIDN:CAA38068.1; PID:g35790
A/Note: the sequence from Fig. 5B is inconsistent with that from Fig. 5A in having 568-T

Best Local Similarity 27.0%; Pred. No. 8.1e-05;
Matches 63; Conservative 35; Mismatches 74; Indels 61; Gaps 13;

QY 1 MALRRPRRLCARLPDFLLLLFRGCLIGAVNLKSSNTPVQEFSEVELSCIITDSQT 60
DB 2428 LSVHGPTVS---LPE-----GPAHVKG-----KDTLLEICSSGEPR 2463

QY 61 SDPRLEWKKIOEQTYVFFDNKIOGDLGRAEILGKTSIKIWNTRDSALYRCEVVAR 120
DB 2464 SSFR--W-----TRLCIPKLEPRMGCLMN--SHMLKIASVKSPSAGTYVCO--AQ 2509

QY 121 N---DRKEIDIVIELTVQKRPVPCVPA---VPVGMATLHQESGHPRHYSW 173
DB 2510 NALGTAKQGV-ELIYD-TGTVAAGTPQVQVESELTEAGHTATLHC--SATGNPPTIHW 2566

QY 174 YANDVPLPTDSRANPRFRNSSSHINSEGTIVFTAVHKDSCGYCIASNDNG 226
DB 2567 SKLRAPLPWQHRI-----EGNTLVIPRVAQDSQYICMATNSAG 2606

RESULT 14

neural cell adhesion molecule short domain form precursor - bovine

N:Alternate names: NCAM-140

C:Species: Bos primigenius taurus (cattle)

C>Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 22-Jun-1999

C:Accession: A33976; A38778; B44290; S05402

R:Rabin, V.M.; Khramtsov, N.V.; Andreeva, S.G.; Moshnyakov, M.V.; Petukhova, G.V.; Raki

FBBS Lett. 254, 69-73, 1989

A:Title: Calmodulin-independent bovine brain adenylate cyclase. Amino acid sequence and

A:Reference number: A32976; PMID:2776887

A:Accession: A32976

A:Molecule type: mRNA

A:Residues: 1-853 <LIP>

A:Cross-references: GB:X16451; NID:960; PIDN:CAA34470.1; PID:961

A:Accession: A38778

A:Molecule type: protein

A:Residues: 20-35;51-61;113-117;122-147;155-161;262-275;279-302;353-360;369-382;544-562;

A>Note: the authors identified this protein as calmodulin-independent adenylate cyclase

R:Roudon, G.; Marshak, D.R.

J. Biol. Chem. 261, 3396-3401, 1986

A:Title: Structural and immunological characterization of the amino-terminal domain of m

A:Reference number: A44290; PMID:86140120; PMID:3512556

A:Accession: B44290

A:Molecule type: protein

A:Residues: 20-36 <ROU>

A>Note: 23-Glu was also found

C:Comment: NCAM mediates cell-cell adhesion via homophilic binding with another NCAM mol

C:Comment: Various forms of NCAM are produced by alternative splicing.

C:Superfamily: neural cell adhesion molecule; fibronectin type III repeat homology; immu

C:Keywords: alternative splicing; brain; cell adhesion; duplication; heparin binding; s

F:1-19/Domain: signal sequence #status predicted <SIG>

F:20-853/Product: neural cell adhesion molecule, short domain form #status experimental

F:20-719/Domain: extracellular #status predicted <EXT>

F:334-98/Domain: immunoglobulin homology <IMM1>

F:132-191/Domain: immunoglobulin homology <IMM2>

F:152-156/Region: heparin binding #status predicted

F:161-165/Region: heparin binding #status predicted

F:228-288/Domain: immunoglobulin homology <IMM3>

F:261-270/Region: NCAM binding #status predicted <IMM4>

F:321-396/Domain: immunoglobulin homology <IMM5>

F:428-490/Domain: immunoglobulin homology <IMM5>

F:527-604/Domain: fibronectin type III repeat homology <FN3A>

F:633-693/Domain: fibronectin type III repeat homology <FN3B>

F:720-737/Domain: transmembrane #status predicted <INT>

F:738-853/Domain: intracellular #status predicted <INT>

F:41-96,139-189,235-266,328-346,435-488/Diulfide bonds: #status predicted

F:222,314,346,432,458,487/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match 10.0%; Score 163.5; DB 1; Length 853;
Best Local Similarity 27.3%; Pred. No. 1.7e-05;
Matches 63; Conservative 34; Mismatches 89; Indels 45; Gaps 11;

QY 27 CLIGA-----VNLKSNR-----TPVQEFSEVELSCIITDSQTS-DPRLEWKIQ 71
DB 96 CVTAEADGTESEATNVNLIKPKLMKNAPTPEFREGDAVAVCGVSSLPETIIMK--- 152

QY 72 DEQTYVFFDNKIOGDLGRAEILGKTSIKIWNTRDSALYRCE--VVARNDKEIDEI 129
DB 153 -----HKRDVILKDV--RFVLTNNYLOIRGIKTEGTGRCGRILARG---EINFK 202

QY 130 VIELTVQKRPVTPVCR--VPKAVPVGMATLHQESGHPRHYSWYRNDVPLPTDSRAN 187
DB 203 DIQVAVNPPTVQARQSVNATANLQSVTLVC--NAGPPEPTVSWTQDGEQIENEBDEK 261

QY 188 PFRNSSSHINSEGTIVFTAVHKDSCGYCIASNDGASARCEQEMEYV 238
DB 262 YIFSDSSE-----LTIRVNDKNDDEAVYCIANKKG-----EQDASIH 300

RESULT 15

protein UNC-89 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 03-Dec-1999

C:Accession: T29757

R:Du, Z.; Le, T.T.; Wilson, R.

submitted to the EMBL Data Library, May 1997

A:Description: The sequence of C. elegans coemid C09D1.

A:Reference number: Z20679

A:Accession: T29757

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-6642 <DUZ>

A:Cross-references: EMBL:AF003131; PIDN:AMB54132.1; GSPDB:GN00019; CESP:unc-89

A:Experimental source: strain Bristol N2; clone C09D1

C:Genetics:

A:Gene: CESP:unc-89

A:Map position: 1

A:Introns: 17/2; 108/3; 154/2; 211/2; 265/3; 326/2; 352/3; 426/2; 454/1; 500/1; 537/1; 6

/3; 5917/1; 6027/1; 6061/3; 6153/2; 6515/1; 6552/3; 6609/1

Query Match 9.9%; Score 162.5; DB 2; Length 6642;

Best Local Similarity 21.6%; Pred. No. 0.00024;

Matches 71; Conservative 39; Mismatches 93; Indels 125; Gaps 12;

QY 45 EFSEVELSCIITDSQTS-----DPRLEWK--IQDQTYVFFDNKIOGDLGRA 92
DB 3828 EFVELNSCTVTEKQOALIKCKVGEPRPKIKWTEGKEVMSARVARAEHDDGTL----- 3883

QY 93 EILGKTSIKIWNTRDSALYRCE-----VVARNDKEIDEIVIELTVQVK 138
DB 3884 -----TLTPNVQADAGEYRCEAENYGSAMTEGPIIVTLGAPKIDGAPDLQPVK 3937

QY 139 PVTVCVRAVPKAVPVGMATLHQESGHPRHYSWYRNDVPLPTDSRANPRFRNSSSHLN 198
DB 3938 PA-----VVTGFTVLELGKIS--GKPKPSVMKYGKSEL-----KPSDRVYIENLD 3982

QY 199 SETGLVFTAVHKDSCGYCIASNDG-----SARCEQ 233
DB 3983 DGTQRLVTNANKLDDMEYRCEASNEFEDVWSVTLVYKEPAQVAPGFKELSAIQVET 4042

QY 234 EMEVYDNLIGGILIGVLVAVLALTLGICCAVRRGYFINNKDGESEYKPKGRP----- 288
DB 4043 ETAKFEKCVSG-----TKPDVKMKFKD-GTPLEMDK 4071

QY 289 -----DGVNYI-----RTDEGDFR 303
DB 4072 RVHESTDDGQRLVIEDSKTDGQNYR 4099

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